

GenCore version 5.1.6  
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OK protein - protein search, using sw model

Run on: June 17, 2004, 14:15:01 ; Search time 24 Seconds  
(without alignments)  
452.902 Million cell updates/sec

Title: US-09-441-242a-2

Sequence: 1 AECPTLGEAVTDHPDRLMAW.....VYHKKDGEVMDLLELPDD 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	612	100.0	114	2	138286	T cell leukemia/ly
2	221	36.1	107	2	S78532	MTCP-1 protein spi
3	86	14.1	618	2	AC0884	glutathionylsperm
4	83	13.6	619	2	A91113	glutathionylsperm
5	83	13.6	619	2	A85958	glutathionylsperm
6	83	13.6	619	2	A57538	glutathionylsperm
7	75	12.3	275	2	F81675	conserved hypotet
8	74	12.1	363	2	S74814	hypothetical prote
9	73.5	12.0	196	2	D75554	probable cytochrom
10	72	11.8	377	2	S61892	polyaccharide exp
11	71.5	11.7	727	2	A71069	hypothetical prote
12	69	11.3	687	2	E69733	PBSX prophage ORF
13	69	11.3	1145	2	T13810	DNA-directed DNA p
14	69	11.3	2944	2	A54849	collagen alpha 1(V
15	68	11.1	259	1	PMRBBM	biophosphoglycerat
16	68	11.1	1426	2	T00337	hypothetical prote
17	67	10.9	399	2	B82197	zona occludens tox
18	66.5	10.9	218	2	T15053	ribonuclease (EC 3
19	66.5	10.9	411	2	D75543	aminopeptidase - I
20	66.5	10.9	567	2	T08405	hypothetical prote
21	66	10.8	256	2	HMSA2	H-2 class II histo
22	66	10.8	256	2	I54447	gene MHC H2-I-A-al
23	66	10.8	258	1	HMSA2	H-2 class II histo
24	66	10.8	259	1	PMRBBM	biophosphoglycerat
25	66	10.8	313	2	A45822	beta-lactamase (EC
26	66	10.8	702	2	AG0005	guanosine-3',5'-bi
27	66	10.8	4151	2	G70944	probable polyketid
28	65.5	10.7	399	2	A43864	zona occludens t
29	65.5	10.7	454	2	G70797	hypothetical proteal

30	65	10.6	233	2	I79357	IA-alpha polypept
31	65	10.6	254	2	S11649	class II histocomp
32	65	10.6	259	1	PMRBBM	biophosphoglycerat
33	65	10.6	663	2	A91048	probable 2-compone
34	65	10.6	663	2	B65025	hypothetical prote
35	65	10.6	679	2	B65025	hypothetical prote
36	64.5	10.5	330	2	AF1877	hypothetical prote
37	64.5	10.5	834	2	S66258	glucosidase I - hu
38	64.5	10.5	1534	2	T30295	P-glycoprotein - T
39	64	10.5	266	2	A12762	conserved hypotet
40	64	10.5	271	2	H97543	hypothetical prote
41	64	10.5	312	2	B45335	probable heme A fa
42	64	10.5	334	2	B72033	conserved hypotet
43	64	10.5	334	2	C66593	CT566 hypothetical
44	64	10.5	381	2	A46358	steroid/hydroid ho
45	64	10.5	452	2	AC2718	conserved hypotet

## ALIGNMENTS

### RESULT 1

138286  
T cell leukemia/lymphoma protein TCL1 - human  
N:Alternate names: T-cell leukemia-related protein TCL1  
C:Species: Homo sapiens (man)  
C:Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 05-Nov-1999  
Proc. Natl. Acad. Sci. U.S.A. 91, 12530-12534, 1994  
R:Virgilio, L.; Narducci, M.G.; Isebe, M.; Billips, L.G.; Cooper, M.D.; Croce, C.M.; R  
A:Title: Identification of the TCL1 gene involved in T-cell malignancies.  
A:Reference number: 138286; MUID:95107991; PMID:7809072  
A:Accession: 138286  
A:Molecule type: mRNA  
A:Residues: 1-114 <RES>  
A:Cross-references: EMBL:X82240; NID:G624960; PIDN:CA57708.1; PID:G624961  
C:Genetics:  
A:Gene: GDB:TCL1  
A:Cross-references: GDB:250785  
A:Map position: 14q32.1-14q32.1

Query Match 100.0%; Score 612; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1e-59;  
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	AECPTLGEAVTDHPDRLMAWKEFYLDKQAMVPLTEIKDRQLRVLLRREDEVIGRP 60
Db	2	AECPTLGEAVTDHPDRLMAWKEFYLDKQAMVPLTEIKDRQLRVLLRREDEVIGRP 61
Qy	61	MTPTQIGPSLLPIWMOIYPGGRVSSSPFRLVYHKKIDGVEVMDLLELPDD 113
Db	62	MTPTQIGPSLLPIWMOIYPGGRVSSSPFRLVYHKKIDGVEVMDLLELPDD 114

### RESULT 2

S78532  
MTCP-1 protein splice form BI - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
A:Accession: S78532  
R:Stern, M.H.; Soulier, J.; Rosenzweig, M.; Nakahara, K.; Canki-Klain, N.; Aurias, A.;  
Oncogene 9, 2475-2483, 1993  
A:Title: MTCP-1: a novel gene on the human chromosome Xq28 translocated to the T cell  
A:Reference number: 138045; MUID:9336950; PMID:8361760  
A:Accession: S78532  
A:Molecule type: DNA  
A:Residues: 1-107 <STR>  
A:Cross-references: EMBL:Z24459; NID:G2252491; PIDN:CAA80828.1; PID:G2252492  
C:Genetics:  
A:Gene: MTCP-1  
A:Introns: 35/3; 92/3  
C:Keywords: alternative splicing; T-cell proliferation

Query Match 36.1%; Score 221; DB 2; Length 107;  
Best Local Similarity 40.2%; Pred. No. 5.3e-17; Indels 2; Gaps 1;  
Matches 43; Conservative 23; Mismatches 39; Indels 2; Gaps 1;

Db 7 GEAVTDHPRLMAMEKEFYLDKQHAMLP-TEIKRDLQRLVLRREDVVLGRPM-TPTQIGPS 66  
3 GEDVGAPPDHLMVHGEIYRDEYQRTWAVAVEEERSFLRANV--QGIQVPLGDAAARSHL 60

Qy 67 GPSLIPIMWOLYPPGRKRRSSDSFWRVLYHIKIDGVEDMLLELPDD 113  
61 LTSQLPLMWOLYPPERYMDNNSRLWQIOHMLMVGVCQLIKLPLDD 107

RESULT 3  
AC0884  
glutathionylspermidine synthetase/amidase [imported] - *Salmonella enterica* subsp. *enterica*  
C/Species: *Salmonella enterica* subsp. *enterica* serovar *Typh*  
A/Note: this species has also been called *Salmonella typhi*  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C/Accession: AC0884  
R/Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.  
A/Authors: Parry, C.; Onall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A/Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar  
A/Reference number: AB0502; MUID:21534947; PMID:11677608  
A/Accession: AC0884  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-618 <PAR>  
A/Cross-references: GB:AL513382; PIDN:CAD02971.1; PID:G16504219; GSPDB:GN00176  
C/Genetics:  
A/Genes: STY3310

Query Match 14.1%; Score 86; DB 2; Length 618;  
Best Local Similarity 29.7%; Pred. No. 0.26; Indels 6; Gaps 3;  
Matches 22; Conservative 20; Mismatches 26; Indels 6; Gaps 3;

Qy 16 RLWAM---EKFYLDKQHAMLP-TEIKRDLQRLVLRREDVVLGRPM-TPTQIGPS 69  
439 KTWAMETAFQIREVSREFAAVPIRTGHPQNEVRLLIDVLRPEVLVFEPLMTVTPGNKA 498

Db 70 LPLPMWOLYPPGRY 83  
499 ILPLMWSLFPNHR 512

RESULT 4  
A91113  
glutathionylspermidine synthetase/amidase [imported] - *Escherichia coli* (strain O157:H7)  
C/Species: *Escherichia coli*  
C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C/Accession: A91113  
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasarara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
A/Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gene  
A/Reference number: A99629; MUID:21156231; PMID:11258796  
A/Accession: A91113  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-619 <HAY>  
A/Cross-references: GB:BA00007; PIDN:BA837296.1; PID:G13363345; GSPDB:GN00154  
C/Genetics:  
A/Experimental source: strain O157:H7, substrain RMD 0509952  
A/Genes: EC63873

Query Match 13.6%; Score 83; DB 2; Length 619;  
Best Local Similarity 28.4%; Pred. No. 0.55; Indels 6; Gaps 3;  
Matches 21; Conservative 21; Mismatches 26; Indels 6; Gaps 3;

Qy 16 RLWAME---KPYVLDKQHAMLP-TEIKRDLQRLVLRREDVVLGRPM-TPTQIGPS 69

Db 440 KTWAMETAFQIREVSDREFAAVPIRTGHPQNEVRLLIDVLRPEVLVFEPLMTVTPGNKA 499

Qy 70 LPLPMWOLYPPGRY 83  
500 ILPLMWSLFPNHR 513

RESULT 5  
A85958  
glutathionylspermidine synthetase/amidase [imported] - *Escherichia coli* (strain O157:H7)  
C/Species: *Escherichia coli*  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C/Accession: A85958  
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Iller, L.; Grobeck, E.O.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A/Reference number: A85480; MUID:21074935; PMID:11206551  
A/Accession: A85958  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-619 <STO>  
A/Cross-references: GB:AE005174; NID:G12517552; PIDN:AA658125.1; GSPDB:GN00145; UMG:243  
A/Experimental source: strain O157:H7, substrain EDL933  
C/Genetics:  
A/Genes: gsp

Query Match 13.6%; Score 83; DB 2; Length 619;  
Best Local Similarity 28.4%; Pred. No. 0.55; Indels 6; Gaps 3;  
Matches 21; Conservative 21; Mismatches 26; Indels 6; Gaps 3;

Qy 16 RLWAME---KPYVLDKQHAMLP-TEIKRDLQRLVLRREDVVLGRPM-TPTQIGPS 69  
440 KTWAMETAFQIREVSDREFAAVPIRTGHPQNEVRLLIDVLRPEVLVFEPLMTVTPGNKA 499

Db 70 LPLPMWOLYPPGRY 83  
500 ILPLMWSLFPNHR 513

RESULT 6  
A57538  
glutathionylspermidine synthetase/amidase - *Escherichia coli* (strain K-12)  
C/Species: *Escherichia coli*  
C/Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 01-Mar-2002  
C/Accession: A57538  
R/Bollinger Jr., J.M.; Kwon, D.S.; Hulsman, G.W.; Kotler, R.; Walsh, C.T.  
J. Biol. Chem. 270, 14031-14041, 1995  
A/Title: Glutathionylspermidine metabolism in *Escherichia coli*. Purification, cloning, c  
A/Reference number: A57538; MUID:95294007; PMID:7775463  
A/Accession: A57538  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-619 <BOL>  
A/Cross-references: GB:U23148; NID:9661185; PIDN:AA643339.1; PID:9661186  
R/Baltcher, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C  
A/Title: The complete genome sequence of *Escherichia coli* K-12.  
Science 277, 1453-1462, 1997  
A/Reference number: A64720; MUID:97426617; PMID:9278503  
A/Accession: B65085  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-619 <BLAT>  
A/Cross-references: GB:AE000381; GB:U00096; NID:92367181; PIDN:AA676024.1; PID:G1789361;  
A/Experimental source: strain K-12, substrain MG1655  
C/Genetics:  
A/Genes: gsp  
C/Keywords: multifunctional enzyme

Query Match 13.6%; Score 83; DB 2; Length 619;  
Best Local Similarity 28.4%; Pred. No. 0.55; Indels 6; Gaps 3;